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FEB 1 2002
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/645,415A

DATE: 01/29/2002
TIME: 14:21:10

Input Set : A:\8002059999.app
Output Set: N:\CRF3\01292002\I645415A.raw

P.S.

4 <110> APPLICANT: Bermudes, G.
 5 King, I.
 6 Clairmont, C.
 7 Lin, S.
 8 Belcourt, M.
 10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 11 TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
 14 <130> FILE REFERENCE: 8002-059
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/645,415A
 C--> 16 <141> CURRENT FILING DATE: 2000-08-24
 16 <150> PRIOR APPLICATION NUMBER: 60/157,581
 17 <151> PRIOR FILING DATE: 1999-10-04
 19 <150> PRIOR APPLICATION NUMBER: 60/157,637
 20 <151> PRIOR FILING DATE: 1999-10-04
 22 <160> NUMBER OF SEQ ID NOS: 61
 24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 26
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: Forward primer
 34 <400> SEQUENCE: 1
 35 gaagatcttc cggaggaggg gaaatg 26
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 44
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Reverse primer
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 51 <213> ORGANISM: Homo sapiens
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 54 <221> NAME/KEY: CDS
 55 <222> LOCATION: (1)...(474)
 57 <400> SEQUENCE: 3
 58 atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat 48
 59 Met Val Arg Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 60 1 5 10 15

ENTERED

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62	gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt	.96
63	Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
64	20 25 30	
66	cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag	144
67	Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
68	35 40 45	
70	ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg	192
71	Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
72	50 55 60	
74	tcc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc	240
75	Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
76	65 70 75 80	
78	atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc	288
79	Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
80	85 90 95	
82	gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg	336
83	Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
84	100 105 110	
86	aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag	384
87	Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
88	115 120 125	
90	aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat	432
91	Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
92	130 135 140	
94	tcc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg	474
95	Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu	
96	145 150 155	
98	taa	477
100	<210> SEQ ID NO: 4	
101	<211> LENGTH: 158	
102	<212> TYPE: PRT	
103	<213> ORGANISM: Homo sapiens	
105	<400> SEQUENCE: 4	
106	Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
107	1 5 10 15	
108	Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
109	20 25 30	
110	Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
111	35 40 45	
112	Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
113	50 55 60	
114	Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
115	65 70 75 80	
116	Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
117	85 90 95	
118	Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
119	100 105 110	
120	Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
121	115 120 125	

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122	Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp		
123	130	135	140
124	Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu		
125	145	150	155
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129	<212> TYPE: DNA		
130	<213> ORGANISM: Artificial Sequence		
132	<220> FEATURE:		
133	<223> OTHER INFORMATION: Forward primer		
135	<400> SEQUENCE: 5		
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138	<210> SEQ ID NO: 6		
139	<211> LENGTH: 29		
140	<212> TYPE: DNA		
141	<213> ORGANISM: Artificial Sequence		
143	<220> FEATURE:		
144	<223> OTHER INFORMATION: Reverse primer		
146	<400> SEQUENCE: 6		
147	ccgacgcgtg aaaggatctc aagaagatc	29	
149	<210> SEQ ID NO: 7		
150	<211> LENGTH: 543		
151	<212> TYPE: DNA		
152	<213> ORGANISM: Artificial Sequence		
154	<220> FEATURE:		
155	<223> OTHER INFORMATION: Fusion construct		
157	<221> NAME/KEY: CDS		
158	<222> LOCATION: (1)...(540)		
160	<400> SEQUENCE: 7		
161	atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct	48	
162	Met Lys Lys Thr Ala Ile Ala Ile Val Ala Leu Ala Gly Phe Ala		
163	1 5 10 15		
165	acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc	96	
166	Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser		
167	20 25 30		
169	gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag	144	
170	Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln		
171	35 40 45		
173	ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt	192	
174	Leu Gln Trp Leu Asn Arg Ala Asn Ala Leu Leu Ala Asn Gly Val		
175	50 55 60		
177	gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg	240	
178	Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu		
179	65 70 75 80		
181	atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat	288	
182	Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His		
183	85 90 95		
185	gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc	336	
186	Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr		

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187	100	105	110	
189	aaa gtt aac ctg ctg ägc gct atc aag tct ccg tgc cag cgt gaa act			384
190	Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr			
191	115	120	125	
193	ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt			432
194	Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly			
195	130	135	140	
197	ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac			480
198	Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn			
199	145	150	155	160
201	cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt			528
202	Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly			
203	165	170	175	
205	att atc gca ctg taa			543
206	Ile Ile Ala Leu			
207	180			
210	<210> SEQ ID NO: 8			
211	<211> LENGTH: 180			
212	<212> TYPE: PRT			
213	<213> ORGANISM: Artificial Sequence			
215	<220> FEATURE:			
216	<223> OTHER INFORMATION: Fusion construct			
218	<400> SEQUENCE: 8			
219	Met Lys Lys Thr Ala Ile Ala Val Ala Leu Ala Gly Phe Ala			
220	1	5	10	15
221	Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser			
222	20	25	30	
223	Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln			
224	35	40	45	
225	Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val			
226	50	55	60	
227	Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu			
228	65	70	75	80
229	Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His			
230	85	90	95	
231	Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr			
232	100	105	110	
233	Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr			
234	115	120	125	
235	Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly			
236	130	135	140	
237	Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn			
238	145	150	155	160
239	Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly			
240	165	170	175	
241	Ile Ile Ala Leu			
242	180			
244	<210> SEQ ID NO: 9			
245	<211> LENGTH: 801			

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Input Set : A:\8002059999.app
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246 <212> TYPE: DNA
 247 <213> ORGANISM: Artificial Sequence
 249 <220> FEATURE:
 250 <223> OTHER INFORMATION: Fusion construct
 252 <221> NAME/KEY: CDS
 253 <222> LOCATION: (1)...(798)
 255 <400> SEQUENCE: 9
 256 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct 48
 257 Met Lys Lys Thr Ala Ile Ala Ala Val Ala Leu Ala Gly Phe Ala
 258 1 5 10 15
 260 acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac 96
 261 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
 262 20 25 30
 264 aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt 144
 265 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
 266 35 40 45
 268 tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa 192
 269 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
 270 50 55 60
 272 gtc aag tgg caa ctc cgt ctc gtt aga aag atg att ttg aga acc 240
 273 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
 274 65 70 75 80
 276 tct gag gaa acc att tct aca gtt caa gaa aag caa aat att tct 288
 277 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
 278 85 90 95
 280 ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act 336
 281 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
 282 100 105 110
 284 ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat 384
 285 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
 286 115 120 125
 288 gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt 432
 289 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
 290 130 135 140
 292 ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc 480
 293 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
 294 145 150 155 160
 296 atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga 528
 297 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
 298 165 170 175
 300 ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc
 301 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
 302 180 185 190
 304 caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg 624
 305 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
 306 195 200 205
 308 aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc 672
 309 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
 310 210 215 220

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/645,415A

DATE: 01/29/2002
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Input Set : A:\8002059999.app
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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59